

-continued

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1.-38. (canceled)

39. A method of determining an error-corrected sequence of a double-stranded target nucleic acid molecule, comprising:

(a) ligating the double-stranded target nucleic acid molecule to at least one cypher polynucleotide, to form a cypher-target nucleic acid complex, wherein the at least one cypher polynucleotide comprises:

(i) a random or partially-random identifier sequence that alone or in combination with an end of the target nucleic acid molecule uniquely labels the double-stranded target nucleic acid molecule; and

(ii) a nucleotide sequence that tags each strand of the cypher-target nucleic acid complex such that each strand of the cypher-target nucleic acid complex has a distinct nucleotide sequence relative to its complementary strand;

(b) amplifying each strand of the cypher-target nucleic acid complex to produce a plurality of cypher-target amplification products from each of a first strand and a complementary second strand of the cypher-target nucleic acid complex;

(c) sequencing the cypher-target amplification products to produce a plurality of first-strand sequencing reads and a plurality of second-strand sequencing reads; and